

RESULT 3

Y13221

LOCUS Y13221 3686 bp DNA linear BCT 28-AUG-1997

DEFINITION *Corynebacterium glutamicum glnA* gene.

ACCESSION Y13221

VERSION Y13221.1 GI:2342561

KEYWORDS *glnA* gene; glutamine synthetase I.

SOURCE *Corynebacterium glutamicum*

ORGANISM *Corynebacterium glutamicum*
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; *Corynebacteriaceae*; *Corynebacterium*.

REFERENCE 1

AUTHORS Jakoby, M., Tesch, M., Sahm, H., Kramer, R. and Burkovski, A.

TITLE Isolation of the *Corynebacterium glutamicum glnA* gene encoding glutamine synthetase I

JOURNAL FEMS Microbiol. Lett. 154 (1), 81-88 (1997)

PUBMED 9297824

REFERENCE 2 (bases 1 to 3686)

AUTHORS Jakoby, M.J.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-1997) M.J. Jakoby, Forschungszentrum Juelich, IBT I, Postfach 1913, 52428 Juelich, FRG

FEATURES Location/Qualifiers

source 1. .3686
/organism="Corynebacterium glutamicum"
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CDS 1274. .2707
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HQSLWKDGKPLFHDSEGYAGLSDIARYYIGGLHHAGAVLAFTNATLNSYHRLVPGFE
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stem_loop 2730. .2769
/note="terminator of glnA"

ORIGIN

Query Match 98.7%; Score 2466.4; DB 14; Length 3686;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 2479; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTCTGTGGGGACGAAAATTGCAACTCTCGTTGTAGCTAGATCAACCCCAACCA 60
Db 401 CTCTGTGGGGACGAAAATTGCAACTCTCGTTGGCTAGCTAGATCAACCCCAACCA 460

Qy 61 AGCACGAAGGGCGTCGATCCCGCAAAGATCGGCGCCATAAATTCACTCAAGACAAAT 120
Db 461 AGCACGAAGGGCGTCGATCCCGCAAAGATCGGCGCCATAAATTCACTCAAGACAAAT 520

Qy 121 TACCCGCGGATAACTGCAGTCCCGTTGCCTTGTCTGGAGCCACGGCCGTAGCATCC 180
Db 521 TACCCGCGGATAACTGCAGTCCCGTTGCCTTGTCTGGAGCCACGGCCGTAGCATCC 580

Qy	181	ACCATCACGGCAGGCAGAATCAAATGGTCAGCAGTGGACGAACCAGCGCACGCCACCAA	240
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Qy	241	CCCACACGGCTCCTCTGCATCCACACCGCGCAAGGCCATGCCAACACGGCATGACCTGGG	300
Db	641	CCCACACGGCTCCTCTGCATCCACACCGCGCAAGGCCATGCCAACACGGCATGACCTGGG	700
Qy	301	GTGCGAGCAAAGATCCATCCCGTAGCCAACCCAGGATCACGAAAATAATGAGCGTGGAT	360
Db	701	GTGCGAGCAAAGATCCAACCGTAGGCCAACCCAGGATCACGAAAATAATGAGCGTGGAT	760
Qy	361	GTCGCTACATCGCCCAGCACATCCGTGAAATTGGACAGCACAATAGCAATAACCCAGGAA	420
Db	761	GTCGCTACATCGCCCAGCACATCCGTGAAATTGGACAGCACAATAGCAATAACCCAGGAA	820
Qy	421	ACACCCCAGTCCACGCAGACCCCGCCGATACGACGAGCCACTGAGGACAGAGAGCCGGCC	480
Db	821	ACACCCCAGTCCACGCAGACCCCGCCGATACGACGAGCCACTGAGGACAGAGAGCCGGCC	880
Qy	481	CCTTCTTGAGGAAGCCCCAACCTTCGCCAGGCCACCTGCCGGCGCATCAGGATCGTCA	540
Db	881	CCTTCTTGAGGAAGCCCCAACCTTCGCCAGGCCACCTGCCGGGTGCATCAGGATCGTCA	940
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Qy	601	ATCAAATCCAAACATGTAGAGGGCGGATACTGCAGTCAGTCAAAGGCCTTGCTTAGACGTC	660
Db	1001	ATCAAATCCAAACATGTAGAGGGCGGATACTGCAGTCAGTCAAAGGCCTTGCTTAGACGTC	1060
Qy	661	GCAAAGCGCAATTCTACCTTAAGATCTAACCTTAAGATCCTAACCTGTTGAGGTAGCCACAATTTC	720
Db	1061	GCAAAGCGCAATTCTACCTTAAGATCTAACCTGTTGAGGTAGCCACAATTTC	1120
Qy	721	GAAAAGTTTGATAGATCGACAGGTAAATGCATTATACTGACAACTGCGCAAGGACTACAT	780
Db	1121	GAAAAGTTTGATAGATCGACAGGTAAATGCATTATACTGACAACTGCGCAAGGACTACAT	1180
Qy	781	TTGCAGCCAAGTCTACTACTTGATCTCAAGTCAGCAATTGAAACAAAGCTACAAAT	840
Db	1181	TTGCAGCCAAGTCTACTACTTGATCTCAAGTCAGCAATTGAAACAAAGCTACAAAT	1240
Qy	841	AAACCGTCCACCCATGTCAATGAGGAGTCACCGTGGCTTGAAACCCCGAAGAAATT	900
Db	1241	AAACCGTCCGCCATGTCAATGAGGAGTCACCGTGGCTTGAAACCCCGAAGAAATT	1300
Qy	901	GTCAAGTTCATCAAGGATGAAAACGTCGAGTTGCTTGACGTTGCTTCACCGACCTCCC	960
Db	1301	GTCAAGTTCATCAAGGATGAAAACGTCGAGTTGCTTGACGTTGCTTCACCGACCTCCC	1360
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Db	1361	GGCACCGAGCAGCACTTCAGCATCCAGCTGCCAGCTTCGATCGAGATACAGTCGAAGAA	1420
Qy	1021	GGTCTCGCATTCGACGGATCCTCGATCCGTGGCTTCACCCACGATCGACGAATCTGACATG	1080
Db	1421	GGTCTCGCATTCGACGGATCCTCGATCCGTGGCTTCACCCACGATCGACGAATCTGACATG	1480
Qy	1081	AATCTCTGCCAGACCTCGAACGGCCACCCCTGATCCATTCCGAAGGAAAGACCCCTG	1140
Db	1481	AATCTCTGCCAGACCTCGAACGGCCACCCCTGATCCATTCCGAAGGAAAGACCCCTG	1540
Qy	1141	AACGTTAAGTTCTCGTTACGATCCTTCACCCCGAGGCATTCTCCCGCACCGC	1200
Db	1541	AACGTTAAGTTCTCGTTACGATCCTTCACCCCGAGGCATTCTCCCGCACCGC	1600
Qy	1201	AACGTTAAGTCTCGTTACGATCCTTCACCCCGAGGCATTGCAAGACACCTGCAAC	1260

Db	1601	AACGTGGCACGCAAGGCAGAGCAGTACCTGGCATCCACCGCATTGCAGACACCTGCAAC	1660
Qy	1261	TTCGGGCCAGGCTGAGTCTACCTCTCGACTCCGTTCGTACTCCACCGAGATGAAC	1320
Db	1661	TTCGGGCCAGGCTGAGTCTACCTCTCGACTCCGTTCGTACTCCACCGAGATGAAC	1720
Qy	1321	TCCGGCTCTACGAAGTAGATAACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAAC	1380
Db	1721	TCCGGCTCTACGAAGTAGATAACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAAC	1780
Qy	1381	CTCGACGGAACCCAAACCTGGCGAAAGAACCGCGTCAAGGGTGGTACTTCCCAGTA	1440
Db	1781	CTCGACGGAACCCAAACCTGGCGAAAGAACCGCGTCAAGGGTGGTACTTCCCAGTA	1840
Qy	1441	GCACCATAKGACCAAACCGTTGACGTGCGCGATGACATGGTCGCAACCTCGCAGCTCC	1500
Db	1841	GCACCATAKGACCAAACCGTTGACGTGCGCGATGACATGGTCGCAACCTCGCAGCTCC	1900
Qy	1501	GGCTTCGCTCTTGAGCGTTCCACCAACGAAGTCGGTGGCGGACAGCAGGAATCAACTAC	1560
Db	1901	GGCTTCGCTCTTGAGCGTTCCACCAACGAAGTCGGTGGCGGACAGCAGGAATCAACTAC	1960
Qy	1561	CGCTTCAACACCATGCTCCACGCCAGATGATATCCAGACCTCAAGTACATCATCAAG	1620
Db	1961	CGCTTCAACACCATGCTCCACGCCAGATGATATCCAGACCTCAAGTACATCATCAAG	2020
Qy	1621	AACACCGCTCGCCTCACGGCAAGGCTGCAACCTCATGCCTAAGCCACTGGCTGGCGAC	1680
Db	2021	AACACCGCTCGCCTCACGGCAAGGCTGCAACCTCATGCCTAAGCCACTGGCTGGCGAC	2080
Qy	1681	AACGGTTCCGGCATGCACGCTACCAAGTCCCTTGGAAAGGACGGCAAGCCACTTCCAC	1740
Db	2081	AACGGTTCCGGCATGCACGCTACCAAGTCCCTTGGAAAGGACGGCAAGCCACTTCCAC	2140
Qy	1741	GATGAGTCCGGTACGCAGGCCTGTCGACATGCCCGCTACTACATGGCGGATCCTG	1800
Db	2141	GATGAGTCCGGTACGCAGGCCTGTCGACATGCCCGCTACTACATGGCGGATCCTG	2200
Qy	1801	CACCAACGCCAGGGCTGTCACCAACGCCAACCTGAACCTCCTACCAACCGCTG	1860
Db	2201	CACCAACGCCAGGGCTGTCACCAACGCCAACCTGAACCTCCTACCAACCGCTG	2260
Qy	1861	GTTCCAGGCTCGAGGCTCAATCAACCTGGTGTACTCACAGCGAACCGTCCGCTGCT	1920
Db	2261	GTTCCAGGCTCGAGGCTCAATCAACCTGGTGTACTCACAGCGAACCGTCCGCTGCT	2320
Qy	1921	GTCCGTATCCAATCACCGATCCAACCCAAAGGCAAAGGCCATCGAATTCCCGCTCCA	1980
Db	2321	GTCCGTATCCAATCACCGATCCAACCCGAAGGCCAACCGCATCGAATTCCCGCTCCA	2380
Qy	1981	GACCCATCAGGAACCCATACCTGGCTTCGCAGCGATGATGATGGCCGGCTCGACGGC	2040
Db	2381	GACCCATCAGGAACCCATACCTGGCTTCGCAGCGATGATGATGGCCGGCTCGACGGC	2440
Qy	2041	ATCAAGAACCGCATCGAGGCCACCGCTCCAGTGGACAAGGACCTCTACGAACGCCACCA	2100
Db	2441	ATCAAGAACCGCATCGAGGCCACCGCTCCAGTGGACAAGGACCTCTACGAACGCCACCA	2500
Qy	2101	GAGGAAGCTGCATCCATTCCACAGGCCACCAACCTCCCTGGAAGGCATCCCTGAAGGC	2160
Db	2501	GAGGAAGCTGCATCCATTCCACAGGCCACCAACCTCCCTGGAAGGCATCCCTGAAGGC	2560
Qy	2161	CAGGAAGACACCGACTTCCTCACCGAGTCTGACGTCTCACCGAGGATCTCATCGAGGCG	2220
Db	2561	CAGGAAGACACCGACTTCCTCACCGAGTCTGACGTCTCACCGAGGATCTCATCGAGGCG	2620
Qy	2221	TACATCCAGTACAAGTACGACAACGAGATCTCCCAAGTTCGCTGCGCCAACCCCGCAG	2280
Db	2621	TACATCCAGTACAAGTACGACAACGAGATCTCCCAAGTTCGCTGCGCCAACCCCGCAG	2680
Qy	2281	GAATTGAAATTGACTTCGACTGCTAATTCACTTAGCTAGCGATAGCGGAAACCCCTG	2340

Db 2681 |||||||GAATTCGAATTGTACTTCGACTGCTAATTCACTTAGCTAGCCGATAGCGGAAACCCCTG 2740
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Db 2741 AAATTCTTCATTGAATTTCAGGGGTTCTTTTACATTCCACCTAAAAGGAAAGCGCC 2800
Qy 2401 GGATCCTCCATCATGGTGGATCCGGCGTTTATCTATTTGTTTGGCTAGATGCCGA 2460
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